S02O13

Extension of a citrus genetic linkage map for QTL mapping of freeze tolerance

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Freeze limits the cultivated area of citrus. Periodically freeze events in some producing areas caused severe damages to citrus harvest and low temperature during extreme climate change often affected the citrus global production in recent years. To develop and cultivate freeze tolerant cultivars is the most effective way to avoid damages caused by freeze. Cold tolerance is considered a quantitative trait in plant. In this research, QTL mapping was used to find loci and molecular markers putatively related with freeze tolerance in citrus. A new linkage map was established by combining the segregating data of markers in a published map and SSR markers newly developed from citrus EST and clementine BAC-end sequences. New map integrated 452 SSR markers with 9 linkage groups and covered 923.3 cM of citrus genome with an average genetic distance at 2.04 cM between adjacent markers. Freeze tolerance of the mapping population of parents and 68 progenies was tested by the method of electrolyte leakage in the end of December after more than one month low temperature hardening and semi-lethal low temperature (LT50) was estimated with logistic equation. The distribution of LT50 in the mapping population was not deviated from a normal distribution. QTL analysis was carried out with Map QTL5.0 software. Four QTLs were indentified at LOD≥3.0 using Multiple QTL Mapping (MQM) procedure, which could explain 29.3%, 23.1%, 44.7% and 21.0% of the phenotypic variation. These QTLs were mapped on the linkage group 2, 4, 3 and 1 respectively. The identified QTL areas and nearby markers should be useful for citrus freeze tolerance research and breeding in the future.

S02O14

Location of a chromosome region linked to Alternaria Brown Spot resistance from the evaluation of triploid mandarin populations

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Alternaria Brown Spot resistance in citrus has been described in diploid progenies as controlled by a single recessive allele (r). The objectives of this study were (1) to map chromosome regions that could be associated to *Alternaria alternata* resistance and (2) to analyse the inheritance of the resistance in triploid families resulting from 2*n* gametes and interploid crosses. Bulk segregant analysis coupled with genome scan (650 Single Nucleotide Polymorphism –SNP– markers genotyped with GoldenGate array) was used to identify genomic regions linked to the *A. alternata* resistance gene using a triploid progeny from a SrXrr cross. The results confirmed the monolocus inheritance of *A. alternata* resistance and revealed 44 SNPs differentiating the resistant and susceptible bulks within a 17 cM region near the centromere on chromosome III. De novo mapping from individual genotyping with 9 markers revealed that the *A. alternata* resistance gene could be located at 9.7 cM from the centromere. Two flanking markers were selected to perform marker assisted selection. Three populations from 2xX2x crosses sharing the female genitor (SrXrr, SrXSr and SrXSS) and one population from a 2xX4x cross (rrXSSrr) were evaluated for *A. alternata* resistance. Segregations indicate that 2xX2x crosses are better to obtain more resistant genotypes for a centromeric gene controlled by a recessive allele than 2xX4x crosses, since less heterozygosity is transmitted by 2*n* gametes than by gametes of doubled-diploids.

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Investigating the parentage of 'Orri' and 'Fortune' mandarin hybrids

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Germplasm characterization is now possible with improved molecular analysis tools with a greater ability to detect polymorphisms. Previously citrus cultivars were primarily described according to their morphological